



1

SEQUENCE LISTING

<110> Rastelli, Luca

Pennica, Diane

<120> NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE
SAME

<130> 10716/57

<140> 09/816653

<141> 2001-03-23

<150> 60/191,532

<151> 2000-03-23

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 598

<212> DNA

<213> Homo sapiens hSTRA6 nucleotide fragment, 5' region

<220>

<221> misc_feature

<222> (92)..(92)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (93)..(93)

<223> n is a, t, c or g

<400> 1
 atgtcccagc cagcaggggaa ccagacctcc cccggggcca cagaggacta ctctatggc 60
 agctggtaca tcgatgagcc ccaggggggg gnngagctcc agccagaggg ggaagtggcc 120
 tcctgccaca ccagcatacc acccggcctg taccacgcct gcctggcctc gctgtcaatc 180
 cttgtgctgc tgctcctggc catgctggtg aggcgcgcgc agctctggcc tgactgtgtg 240
 cgtggcaggc ccggcctgcc cagccctgtg gatttcttgg ctggggacag gccccgggca 300
 gtgcctgctg ctgttttcat ggtcctcttg agtcacctgt gtttgctgct ccccgacgag 360
 gacgcattgc ccttcctgac tctcgctca gcacctagcc aagatgggaa aactgaggct 420
 ccaagagggg cctggaagat actgggactg ttccattatg ctgccctcta ctaccctctg 480
 gctgcctgtg ccacggctgg ccacacagct gcacacctgc tcggcagcac gctgtcctgg 540
 gccaccttg gggccaggt ctggcagagg gcagagtgtc cccaggtgcc caagatct 598

<210> 2

<211> 199

<212> PRT

<213> Homo sapiens hSTRA6 amino terminal polypeptide fragment

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa is any amino acid

<400> 2

Met Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu Asp
 1 5 10 15

Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Xaa Glu
 20 25 30

Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro Pro
 35 40 45

Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu Leu
 50 55 60

Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys Val
 65 70 75 80

Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly Asp
 85 90 95

Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser Ser
 100 105 110

Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr Leu
 115 120 125

Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly Ala
 130 135 140

Trp Lys Ile Leu Gly Leu Phe His Tyr Ala Ala Leu Tyr Tyr Pro Leu
 145 150 155 160

Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly Ser
 165 170 175

Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala Glu
 180 185 190

Cys Pro Gln Val Pro Lys Ile
 195

<210> 3

<211> 1351

<212> DNA

<213> Homo sapiens hSTRA6 nucleotide fragment, 3' region

<220>

<221> misc_feature

<222> (437)..(437)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (438)..(438)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (439)..(439)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (440)..(440)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (441)..(441)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (442)..(442)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (694)..(694)

<223> n is a, t, c, or g

<220>

<221> misc_feature

<222> (867)..(867)

<223> n is a, t, c, or g

<220>

<221> misc_feature

<222> (874)..(874)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (905)..(905)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (908)..(908)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1155)..(1155)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1172)..(1172)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1174)..(1174)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1197)..(1197)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1198)..(1198)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1204)..(1204)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (1295)..(1295)

<223> n is a, t, c or g

<400> 3

tgctacatct cagccttggc cttgtcctgc ttactcacct tcctggctct gatgcgctca	60
ctgggtgacac acaggccttg ttctgggggc agcggggatg gccagttttc atggaacctg	120
ttttctgtcc ccctgccact ccgccccctg gcagggctcc tgggtgcagca gatcatcttc	180
ttcctgggaa ccacggccct ggccttctct gtgctcatgc ctgtgctcca tggcaggaac	240
ctcctgttct tccgttcctt ggagtcctcg tggcccttct ggctgacttt ggccttggct	300
gtgatcctgc agaacatggc agccatttgg gtcttctctg agactcatga tggacacca	360
cagctgacca accggcgagt gctctatgca gccacctttc ttctcttccc cctcaatgtg	420
ctgggtgggtg ccatggnnnn nncctgctcc ccagcattg ccatccgcca cccacccca	480
ggctactaca cgtaccgaaa cttcttgaag attgaagtca gccagtcgca tccagccatg	540
acagccttct gtcctctgct cctgcaagcg cagagcctcc taccaggac catggcagcc	600
ccccaggaca gcctcagacc aggggaggaa gacgaaggat gcagctgcta cagacaaagg	660
actccatggc caaggagct agggccgggg ccancgcgg cagggtcgc tggggtctgg	720
cctacacgct gctgcacaac ccaaccctgc aggtcttccg caagacggcc ctgttgggtg	780

```

ccaatggtgc ccagccctgc tcctccctcc ccggctctcc tcccagcatc acaccagcca      840
tgcagccagc aggtcctccg gatcacngtg gttnggtgga ggtctgtctg cactgggagc      900
ctcangangg ctctgctcca cccacttggc tatgggagag ccagcagggg ttctggagaa      960
aaaaactggt gggttagggc cttggtccag gagccagttg agccagggca gccacatcca     1020
ggcgtctccc taccctggct ctgccatcag ccttgaaggg cctcgatgaa gccttctctg     1080
gaaccactcc agcccagctc cacctcagcc ttggccttca cgctgtggaa gcagccaagg     1140
cacttcctca cccntcagc gccacggacc tntntgggga gtggccggaa agctcccngg     1200
cctntggcct gcagggcagc ccaagtcatg actcagacca ggtcccacac tgagctgccc     1260
acactcgaga gccagatatt tttgtagttt ttatnccttt ggctattatg aaagaggtta     1320
gtgtgttccc tgcaataaac ttgttcctga g                                     1351

```

<210> 4

<211> 325

<212> PRT

<213> Homo sapiens hSTRA6 polypeptide fragment, carboxy terminus

<220>

<221> MISC_FEATURE

<222> (146)..(148)

<223> Xaa represents any amino acid, other, or unkown

<220>

<221> MISC_FEATURE

<222> (232)..(232)

<223> Xaa represents any amino acid, other, or unkown

<220>

<221> MISC_FEATURE

<222> (290)..(290)

<223> Xaa represents any amino acid, other, or unkown

<220>

<221> MISC_FEATURE

<222> (292)..(292)

<223> Xaa represents any amino acid, other, or unkown

<220>

<221> MISC_FEATURE

<222> (302)..(302)

<223> Xaa represents any amino acid, other, or unkown

<220>

<221> MISC_FEATURE

<222> (303)..(303)

<223> Xaa represents any amino acid, other, or unkown

<400> 4

Cys	Tyr	Ile	Ser	Ala	Leu	Val	Leu	Ser	Cys	Leu	Leu	Thr	Phe	Leu	Val
1				5				10						15	

Leu	Met	Arg	Ser	Leu	Val	Thr	His	Arg	Leu	Gly	Ser	Gly	Gly	Ser	Gly
		20					25					30			

Asp	Gly	Gln	Phe	Ser	Trp	Asn	Leu	Phe	Ser	Val	Pro	Leu	Pro	Leu	Pro
	35					40					45				

Pro	Leu	Ala	Gly	Leu	Leu	Val	Gln	Gln	Ile	Ile	Phe	Phe	Leu	Gly	Thr
	50					55					60				

Thr	Ala	Leu	Ala	Phe	Leu	Val	Leu	Met	Pro	Val	Leu	His	Gly	Arg	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65					70					75				80	
Leu	Leu	Phe	Phe	Arg	Ser	Leu	Glu	Ser	Ser	Trp	Pro	Phe	Trp	Leu	Thr
				85					90					95	
Leu	Ala	Leu	Ala	Val	Ile	Leu	Gln	Asn	Met	Ala	Ala	His	Trp	Val	Phe
			100					105					110		
Leu	Glu	Thr	His	Asp	Gly	His	Pro	Gln	Leu	Thr	Asn	Arg	Arg	Val	Leu
		115					120					125			
Tyr	Ala	Ala	Thr	Phe	Leu	Leu	Phe	Pro	Leu	Asn	Val	Leu	Val	Gly	Ala
	130						135				140				
Met	Xaa	Xaa	Xaa	Cys	Ser	Pro	Ser	Ile	Ala	Ile	Arg	His	Pro	Thr	Pro
145					150					155					160
Gly	Tyr	Tyr	Thr	Tyr	Arg	Asn	Phe	Leu	Lys	Ile	Glu	Val	Ser	Gln	Ser
				165					170					175	
His	Pro	Ala	Met	Thr	Ala	Phe	Cys	Ser	Leu	Leu	Leu	Gln	Ala	Gln	Ser
			180					185					190		
Leu	Leu	Pro	Arg	Thr	Met	Ala	Ala	Pro	Gln	Asp	Ser	Leu	Arg	Pro	Gly
		195					200					205			
Glu	Glu	Asp	Glu	Gly	Met	Gln	Leu	Leu	Gln	Thr	Lys	Asp	Ser	Met	Ala
	210					215					220				
Lys	Gly	Ala	Arg	Pro	Gly	Ala	Xaa	Arg	Gly	Arg	Ala	Arg	Trp	Gly	Leu
225					230					235					240
Ala	Tyr	Thr	Leu	Leu	His	Asn	Pro	Thr	Leu	Gln	Val	Phe	Arg	Lys	Thr
			245						250					255	
Ala	Leu	Leu	Gly	Ala	Asn	Gly	Ala	Gln	Pro	Cys	Ser	Ser	Leu	Pro	Gly
			260					265					270		
Ser	Pro	Pro	Ser	Ile	Thr	Pro	Ala	Met	Gln	Pro	Ala	Gly	Pro	Pro	Asp
		275					280					285			

His Xaa Gly Xaa Val Glu Val Cys Leu His Trp Glu Pro Xaa Xaa Gly
 290 295 300

Ser Ala Pro Pro Thr Trp Leu Trp Glu Ser Gln Gln Gly Phe Trp Arg
 305 310 315 320

Lys Lys Leu Val Gly
 325

<210> 5

<211> 6964

<212> DNA

<213> Homo sapiens clone RP11-60L3, Sequencing in Progress, 9 unordered
 pieces; GenBank AC023300, nts 150524 to 157487

<220>

<221> misc_feature

<222> (126)..(126)

<223> n is a, t, c or g

<220>

<221> misc_feature

<222> (128)..(128)

<223> n is a, t, c, or g

<220>

<221> misc_feature

<222> (132)..(132)

<223> n is a, t, c or g

<400> 5

gtcccagcca gcaggaacc agacctccc cggggccaca gaggactact cctatggcag 60

ctggtacatc gatgagcccc aggggggcca ggagctccag ccagaggggt aagtgtggaa	120
ccaccncnca cnetcactct gtcagccatc agaatggggg gatggcagag gttgcaactg	180
gccagggagc agctcctggg caggggctgc taggtctggc tctgccactc atttgctgtg	240
tgaccttggg caagtcacag cctctctggg gttcattcag tctctgcctc tgttacatga	300
gaacaacatc cctcaccctg ctgttaagac acctaaaggct ggtcaccta ggtatgatgt	360
gtgacgtgtt aaaaatacag atgattcaga tctgcagggg tggctccctg ggtgattctg	420
gcccatagcc aggatggaga agctgctgag agcagttgag gcaagcagac ctcccttcaa	480
ggggttattg gtctctgtgg tgagcatttg ggtgtggtgt ttccaagtgt caagttctct	540
gggcaggctg ggggattcgg ggaaggcaga gaaccaaagg gagaaagcct ggtgagaagt	600
cactgaggaa acaagcacc ctgttgtctt tggatggctc cagaggatga ggagagccta	660
ttccctttag cagaagtgtc caggccagcc caggtgaggg tgggagcagg aaggcagccc	720
gccccagggt ggctgagaa cccagccaca gctgctttgc ctgggtccat tctaccgggg	780
tttagtctgg gcaccctggt ggaggagctg ggccccctct gtgtcccca cctcctgcca	840
ggatgtcttg cctgtgtagg acccagagcc agttctcccc tgttggtccc aggcctggcc	900
ccatccctta tctccctgct ctgtctgacg gtttgagaaa gtagaaagggt gaggctgggg	960
gttgccgagc cagatgtgtg cacatctgtt ctccatcaaa acctgaaact tgagaaggaa	1020
aaatccttgc gtgcctcccc aggggctggg gctgcggcct ggctgggctt gggcatcca	1080
gcagggacag aggctccacc caggcctcgg ggaaggagct gttgtttgga ggactcaggg	1140
ttctgaccac ctggaaaata gcctgcagtc agcaagggcg tgctccccac tcatcttgcc	1200
tgactgaccg agagcctgtg ggctccacat atcctgctgt gtatgtgtgg cctgcgagag	1260
accagaatga ggacaggccc aggaacccat gaggatgggt tctgacctag gtgaaggctc	1320
taatctgaag ctgtgtcctt gggagcctca gggcctgggc actggctggg ggccaggtgc	1380
ctgtaaatgt agctgtggtc tatagctgtt gtctcagaat aaagtgtgtg gtatgtcagg	1440
cactgggtga tggggagtcc agtccctcat gtgggtgaca tctagaagat tcagcttctt	1500
tctcccactg cagggcata catccataag aataaagaga tttgtttgaa tctacttact	1560
tagccaaacc aattgagctg cctgccatcc ccctgcccc aaagtgggag cagaaaattg	1620
ggagctcagg ggaatcccaa ggaaatgaac ttgggttcac ctctgtctgt gtgagtcaga	1680

caccctgggg	acatgttgca	tcagagcttt	gaagaactcc	ggagtgccca	gtgccccagc	1740
actctcaggc	tggagttggg	gtggatgaac	actgatggca	gtggagtcag	ccacagaaat	1800
gtcctaaaat	ccagaacatt	caatggctca	aacaccctca	gtggcttcct	ggggcctccc	1860
atgcttgctg	taacctcatc	tcacctgacc	tctgggctgc	aatcaaactg	gaaggcctgc	1920
ccagccccag	ccacgctgcc	tgtcgctgc	ctctctgctt	cctcatgcac	ttccctccac	1980
ctggagctgc	ctctccccct	ctttgcctaa	agagatgcta	accaactttt	atttatttat	2040
tttttgagat	ggagtctcgc	tcttgttgcc	cgggttggag	tgcagtgggtg	cgatcttggc	2100
tcactgcaac	ctccgcttcc	ccagttcaag	tgattctcct	gcctcagcct	cccagtagac	2160
tgggattaca	ggtgcgtgcc	accacgccc	gctaattttt	tttgtatttt	tagtggagac	2220
agggtttcat	catgttggcc	aggctggctc	caaactcttg	accttgggtg	atctgcctgc	2280
ctcagtctcc	caaagtgctg	ggattatagg	cgtgagccac	tgtctccagc	cactaaccat	2340
tttttaaact	ccaatcagat	accacctcct	tttgcccaaa	gttctccctc	ctctgcatcc	2400
ttcagcacct	gctgtgcctg	tcccaggatc	aagctcacca	ccctctccaa	ggtctttatg	2460
tctgtgccat	cctgcctgtc	ccatggcaca	aaaagtgggg	ccacaagcca	ctagccaaat	2520
atttgcctcat	ttctatgcc	cctgagatcc	ccatctgacc	cctcacactg	agctgagagg	2580
tcagatgggg	acctcaggtg	atacaaaaag	ggccagaggc	tccccaggc	agggccctgg	2640
agggcatttc	tgggggtagg	ggtggtttgg	ggtaaggctc	ataggaaaat	ggtcaaaacta	2700
ctccagggac	agttttccaa	gtccctgccg	ggcccagggtg	taaagggtga	gcgggaccta	2760
gtcatgcggg	gagatgccgg	ctgagaggga	gggctgcctc	acgcaccgga	gtgagaggcc	2820
ttggagctgg	aggtggggag	ctgacactgg	agtcagtgtg	gctgtacttc	acgatcccag	2880
ttctactttg	ggaagaggct	ggtctcctgg	ccaagaagct	gccagagct	gacttactct	2940
gcctctccac	caagtgactg	gtttctttcc	caccgctcac	ccgctgggat	ttcctgagag	3000
aaagcgagca	ggacagaccg	agctgaccca	gcagagcatc	ccagggtctc	gcactcccct	3060
ggataatgca	gccttgatgc	ctctcttcat	acagtggagg	gcgttttggt	gggcggctaa	3120
gccctctgtg	caggcaggga	ctggcggcag	cccaggctcc	atctcaggcc	ctcaccacc	3180
agaccccact	ggcctcacc	atgctgccac	cctccctctg	gctctcccag	gccaagctg	3240
ggaaaacccg	gagctctact	gtccaccagg	gaccagctcc	tgcctactct	cccagggcc	3300
gggccagccc	tgagctcagg	actcctgcct	cactcccttt	ctccaccaca	tgattctgct	3360

ggggaagcgg	agggtttcat	tgtcctcagt	gacccctatc	tccactgtgg	gtttacctct	3420
gcgctcagcc	agggtgagt	caggaccatt	gccaggccat	agggagcctc	tgtggaatta	3480
gagaaaggga	tccccagtta	ggtgcattca	gctcagcagg	tgctggggtt	ggtgagcagg	3540
gtggcctgct	cgttccttg	gctgagcatc	tttgtgcagt	gggcaacctg	catggctgtc	3600
catggaggct	ctcaatgaga	gggaagcagg	aaaagagagg	gaccagggga	gatcatttta	3660
gtcacagacc	aacctcagat	ggcagtgagt	agaggggcga	tcacagggcc	aaacccttga	3720
ctgcttgacc	caggtagtgt	gctcaactgc	agttctgaga	agacgtctgt	gagaccagga	3780
gcagtcagag	gggctccctg	gagaggggag	gccttgaagg	acaggaagca	tctgggtgag	3840
caagaataag	tgctcagccg	ggcacagtgg	ctcacacctg	taatcccagc	actttgggag	3900
gctgaggcat	gaggattgct	tgagctcaga	aatccaagac	cagcctgggc	gacatgggtga	3960
ggccctgtct	ctactaaaaa	tacagaaaaa	aaaatgccag	gcatggtggt	gcacacctgt	4020
ggtcccagct	actcatgagg	ctgaggtggg	aggatctttt	gagcccagga	ggctgaggct	4080
gcagtaagcc	gagatcgagc	cactgcactc	cagcctgggt	gacagagcaa	gaccctgtcc	4140
ctccagaaaa	aaaaaaaaaga	gaataagtga	tcaggccgag	ccggtctact	ctgcttcccc	4200
tgggagcttc	ccatgtcctt	tagtcttata	accccagagc	ttggcatggg	gctggcacat	4260
cacaggga	cgaggggccc	agaatgacct	tgagaagggt	ggactgggaa	ggcttgtgta	4320
ggagggatca	gagggttgag	ggaggtagt	ggtaaagcct	cagtgtgaac	agtcttgaac	4380
cccagacca	tctgcacacc	cagggggggc	tgacgcaggc	ctgagccagc	cttcatttgc	4440
tctgcaggga	agtgcctcc	tgccacacca	gcataccacc	cggcctgtac	cacgcctgcc	4500
tggcctcgct	gtcagtgagt	ccaacccaag	ttgaacctgg	cttgcaagct	gctgccagcc	4560
tgggcagtgg	gacctgtgtt	ccccactggg	gctgggtgaag	gggggcccctg	gaagatcctg	4620
ggtgggggga	gctatctggg	agttctccca	gcttggaggc	ccaaaccagg	atgcaagtcc	4680
aaccttccag	atgtctgtca	ccccttgacc	agtccccaag	atgccacatg	agtgtgcact	4740
gggcaggtag	gggatatcct	ggggcctgag	tccaagccct	caaactcaga	ccctcagggg	4800
aggcctgggc	acccaagcc	ctcctctgca	ctctcctttc	agatccttgt	gctgctgctc	4860
ctggccatgc	tggtagggcg	ccgccagctc	tggcctgact	gtgtgcgtgg	caggcccggc	4920
ctgcccaggt	ttgtaccatg	gcctgggcac	ccccactcag	gggacccagc	tgacaggggtc	4980

cctctgggag ggtgggtgat ttgttaggta cctaaaaggc agctctggct ttaatgacat	5040
ccctatcgcc ctacagcctgg agctttcctc acccccacct aggtctccag gtttagtcag	5100
gacccccaga ggaaggggga gggactcgct caagcccgcc tgggagaaag gactccaacc	5160
cagaccctag ggaaacaagc ctgacaggac ccagcgtcag agtgtacctt ctgaggcagc	5220
cctccatgtg tggattgacg tgaccatccc aatgccatct tgaccgtcat cttccctgag	5280
ggtatcacct ggaccctaata gcttgaaggc agatttatgg ggactgacat ctagccccta	5340
tagctggagc tttcttctcc tatctccttc agccctgtga ctccagagcc tggacaggcg	5400
tgatcctgag gagatggggc tgggcaagct agtgtgcgag agaccaaagg gttagggcag	5460
gtgatgggtg gctccttggg gtagacagct tcacatccca gacccagact gtgcaccgag	5520
gcaggctctg ctgtgctggg tttgtgggga accagcctgg ggtctctggg tggccccaga	5580
aagagcttgc cctggctggg gcagtgtttg agggagaatg aacctctcag agcatgaatg	5640
caagctgcag tgcagaagct gtgggtctga gtggcttgcc ctgagcccag aagggtgatg	5700
cctgggacag ctatgcccg tgtctgcct ctgccccggg tccacacca gccagggcg	5760
gcggctgttg tacaaggatg ttgtgactcg ctgagttctc tgaaggtttg ccagctcaga	5820
cagaccaatt agtgtggagg tggctgcttc ctggagcttc caggggtggg ggaggagcag	5880
tcttagggct tcttcccact gtatgtgtgt cccaagtccc tttggcacgg ggcccagagc	5940
ttggtagata agaggcactc cacaaatatc tatggaatga atgaatgaag gggccttatt	6000
ccccatcta gaaagtggga ctgactccac ctcttgatt tatggaatac agctgggagg	6060
taatgggggt gcaggggctg agcaactccc tcctgccctg tccttgctc tgtgctagcc	6120
ctgtggattt cttggctggg gacaggcccc gggcagtgcc tgctgctgtt ttcattggtcc	6180
tcctgagctc cctgtgtttg ctgctccccg acgaggacgc attgcccttc ctgactctcg	6240
cctcagcacc cagccaaggt acccactgac cccaggccc tggggttggg gtgatgggat	6300
ggggtagggg ggggtctcgg agttttaagc ttggctcaag gagatgagag taacaggaac	6360
agctgtcaat gagatgggct gctatcctga gacgtgacct ttttagacca tccagtcttt	6420
acaacgatgc taaaagtat gcatattagc ccattttgc aatggaggaa ctgagagcca	6480
gggaagtagt atcttaaatt gagtatctgc tcaggcacca tgctaagcat tatatatcca	6540
ccttctcatt ttgcccttgc taatatactg tgattatctt cattttacag atgggaaaac	6600
tgaggctcca agaggtaact tgcccaagat cacagagttg agactagtca gagcctggat	6660

ttgaacctag tgttcttgcc cactgaacgt gctgaagggc ttggaagctg gagaccgaag	6720
agaggcctgg gtgggctcac tgcaggcccc atgtctgccc ctccagcatg ggtctctctg	6780
cttgtttcac cttccagggg cctggaagat actgggactg ttctattatg ctgccctcta	6840
ctaccctctg gctgcctgtg ccacggctgg ccacacagct gcacacctgc tcggcagcac	6900
gctgtcctgg gccaccttg ggggccaggt ctggcagagg gcagagtgtc cccaggtgcc	6960
caag	6964

<210> 6

<211> 5585

<212> DNA

<213> Homo sapiens chromosome 15 clone RP11-665J16 map 15, WORKING DRAFT SEQUENCE, 10 unordered pieces, nts 127763 to 133347

<400> 6	
ctcaggaaca agtttattgc agggaaacaca ctaacctctt tcataatagc caaaggcata	60
aaaactacaa aaatatctgg ctctcgagtg tgggcagctc agtgtgggac ctgggtctgag	120
tcatgacttg ggctgccctg caggccagag gcccgggagc tttccggcca ctcccagag	180
aggtccgtgg cgctgagggg gtgaggaagt gccttggtctg cttccacagc gtgaaggcca	240
aggctgaggt ggagctgggc tggagtgggt ccagagaagg cttcatcgag gcccttcaag	300
gctgatggca gagccagggt agggagacgc ctggatgtgg ctgccctggc tcaactggct	360
cctggaccaa ggcctaacc caccagtttc tttctccaga acccctgctg gctctcccat	420
agccaagtgg gtggagcaga gccctcctga ggctcccagt gcagacagac ctccacccaa	480
ccacagtgat ccggaggacc tgctggctgc atggctggtg tgatgctggg aggagagccg	540
gggagggagg aggatggtag gcaggaacat gcctcagcac agatgggcag gtgggttgac	600
cttccctgcc ctgagggtg ggcaccattg gcaccaaca gggccgtctt gcggaagacc	660
tgcagggttg ggttgtgcag cagcgtgtag gccagacccc agcagccct gccgcggctg	720
gccccgggcc tagctccctt ggccatggag tcctttgtct gtagcagctg catccctgag	780
agagacggac tttctgtgag tactcagca aacaccagc caaccctccc tggccctcag	840
acctgatcag agagcctgaa aatcccaggc gtgtgcaggt cgtgaggctt aggatgtccc	900

ctgcaggcag	cacatggaag	tggggggtga	ggctctgtgga	tggactggaa	gctgggtggg	960
acaaggggtct	ggagctggct	tagtgtcccc	tccctacaca	cacttctggg	cagaaggaaa	1020
ggaggagtgca	tactccctgc	ccaagggag	aagcgggggc	agtgacggag	ccccttagga	1080
aggcagctgt	ttcattctct	ctgtgtgcac	acatatggtg	tgtgtatgtg	tgtgttcata	1140
tcatggaaaa	aatcaccctg	agatcagacc	aggaggggtg	accaaaggca	gccaaggaag	1200
agaggaagtg	agaattttcc	tggcgctcac	tctgtgtgct	ggggaggggc	acacatcctt	1260
cctagaagaa	gctgggtagg	ctctattccc	ccattcccag	tgggagggcg	caccttcgtc	1320
ttcctccctt	ggctctgaggc	tgtcctgggg	ggctgccatg	gtcctgggta	ggaggctctg	1380
cgcttgccagg	agcagggagc	agaaggctgt	catggctgga	tgcgactggc	tgacttcaat	1440
cttcaagaag	tttcggtacg	tgtagtagcc	tggggtgggg	tggcggatgg	caatgctggg	1500
ggagcagggg	ccacactgga	ggcatccaga	catcccctaa	cacacacaca	gggagtgcac	1560
gtgcactccc	tgcattccaag	catgtcgaca	caccaagcac	gtggcacatt	ggctgcatgg	1620
gcacgtgtgg	acctgctaga	acaccccaca	tccactgcac	gtgctgcagg	gccacaggag	1680
gcacagcgca	ggggcacaca	ggtggcacat	gcagctacag	gcatcggtgt	gaactgatca	1740
gctggcacgg	ccctggggca	gggcagatgc	cttcctcact	gcttgggtag	cctgagcaat	1800
cctccagccc	cgcccagtga	ccttaccggg	gtcgagagtg	gcggctctcg	gtggcagcag	1860
gctgaggtcc	atctggccaa	ggtggatggc	gttgtagagg	gcagagagga	gcactcgcca	1920
ggtggccacc	atggcaccca	ccagcacatt	gagggggaag	agaagaaagg	tggctgcata	1980
gagcactcgc	ctaggatggg	agaagaaagc	tgaggcaggc	cgttccccag	agctccctcc	2040
ccagggtcag	tgtcagacct	ggatgccag	aactgctgtg	tatttactga	gtgcctacca	2100
tttattgcta	tgtcttctgt	gcaccccacc	ctgggcaagg	ccttctctct	ttcaaccac	2160
catgctggga	gatgggaaac	tgaggcccag	agagattggg	agacttagcc	aaggctgtca	2220
gctattcagt	ggcagagctg	ggctttaact	ctaggtccat	ctgagtcttt	ctatgaccct	2280
gatgcctccc	acctcccttt	tctgggtccc	ctgtctgcta	attccaagtt	cccctgggag	2340
ccaaggttct	cccacagact	tgtcatctga	cagggaaactc	ccttgctaca	aagtggggag	2400
gggcatggtt	ttaaggaaac	agaggatcca	ggggagagca	gtaccgattc	ccaaagcaag	2460
aaaggttcac	gggggtactt	ccagccccat	gccgggtatg	tagagaggta	ctttggagtg	2520

ggctgagcca	ttgtcccttt	tctctatggg	taaggcaagc	tctttctact	atcatctggg	2580
ttccttgata	gagagaaggg	atagatggca	gtggagggag	gacacaaaaa	gagagagaca	2640
ccgaagaaga	ggcgagggcc	tgagggagcc	acaagcccag	atgccacctc	accggttggt	2700
cagctgtggg	tgtccatcat	gagtctccag	gaagacccaa	tgggctgcca	tgttctgcag	2760
gatcacagcc	agggccaaag	tcagccagaa	gggcctgcca	gtgggggtggg	gaggtggtcg	2820
ctgttagcgg	acctctaagg	agtccctgag	ccctccatgt	cttgtttcac	tcaccacgag	2880
gactccaggg	aacggaagag	caggaggttc	ctgccatgga	gcacaggcat	gagcaccagg	2940
aagggcaggg	ccgtgggttc	caggaagaag	atgatctgct	gcaccaggag	ccctgccagg	3000
ggcgggagtg	gcagggggac	agaaaacagg	ttccatgaaa	actggccatc	cccgtgccc	3060
ccagaaccaa	gggctttggg	attgggcagg	cctggtttta	gatctctgct	ctgccactgc	3120
ctagctatgc	tgccttgaac	aaatcacttt	acttcattga	gcctcagttt	cttcctctgt	3180
aaaatgggga	taatagtccc	tacctcagag	gctgttgtaa	ggatccaatg	agataatgtc	3240
tgtggaaact	cttaaaatca	caaaatactt	tgcaaagtgt	atttccctcc	agtttctcct	3300
gagtttgagt	tactggggga	taaggctaca	tattaaactg	atgtttgcat	tccttcaagc	3360
cagagcctgg	catacggtag	gtgcccgaag	actgtctatt	gaaataatct	ggccaactga	3420
ttagagaatg	atgtctacaa	aagggcctgg	aggcataagg	gctaccaaga	agagacgcta	3480
tgacttttgt	cctagtaatt	catctactcc	tttaccatcc	ttctcctccc	gcaaggaggt	3540
gagaatggaa	ggaactggag	ggagagatac	aaggcccttg	gatgtgcaac	ccaggccaca	3600
gcccctcacc	attcagagtg	cttttctcac	tgcagtaccc	aaggggagag	tcagaaactt	3660
ggggctggta	ggggtcctgg	aaggttatct	ggtccaactc	tctcagggca	ggaccccctt	3720
tgcagactgc	aacaatatcc	atggaactct	gcttgcatac	ccccagtgac	agggatctca	3780
ttacctttgt	aggtagccaa	atgtgacaca	gccctttctt	aagctggagc	gcagtgggtg	3840
aatctcggct	cactgcaacc	tccacctcct	gggttcaagc	gattctcctg	cctcatcctc	3900
ccgaatagct	ggaactgcag	gtgcacacca	ccatacccg	ctaatttttg	tatttttagt	3960
agagacgggg	tctcaccatg	ttggccaggc	tggcttctat	ctcctgactt	cgtgatccac	4020
ctgcctcagc	ctcccaaagt	gctgggatta	caggtgtgag	ccactgagcc	cagccaggaa	4080
tgtaccattt	tgaatttgac	acctccagac	ctgggtccac	ccccatgtga	atacttggtg	4140
gcacccaggg	ttcatctcca	tgtggagggg	acacactcaa	tttcccagg	gctcctgtac	4200

```

ccccatcctg aataagcttc ttaagggcag ggaaggcagg ggggtccctc cttcttgctg 4260
ctgccccaga gcattcccag acaaactctg agggcagtag ttgctgagca ctcttctccc 4320
caactgaggc cagtgtctga ggggaggccc aggccaaaggc tgggtgtggc gggcaaggga 4380
ggctcaccaa ggcagataaa ggctgtctgg taggcactga agctcatcca acagaatatg 4440
gcttggcggg agggatgggg actccgatgc aagggactca agtccagggc agctcctcgg 4500
tgcagagctc gaaggttggg cctgggggtg gagccagggg ggcagagacc tcaggagagca 4560
acacactctt cctaaatcct cctctggggc agcaactggc caaactccca atagaatttc 4620
aactcacagc catcagcagg gaagcccaga actgtgggag ccaggaggag gccactaacc 4680
caagatatct ggaagaggtg atatctgggt agtcttaaac agtgaacgag gaatacaaaa 4740
cgaggcagaa ggctcaacct gagccaagtc agaaaagtga gaaacaacag tgagaatgga 4800
agtgacacac agcacagcca acaggtaaag aggcaaggca agcacaggct gaggagcctt 4860
gaatgccaga agaaggaggg gtgacctgtg gaaaaagatc cctgggaaga gctctgagac 4920
ctggcaagtg cgcaggagac atgggccagt tctctgacat gggtaagtgc tcgggctgcc 4980
ccttccacct gccctgggac ttcagtgtc ctcaccactc accgctgcag ggcaagcaag 5040
gtggcatggc gagaccgta ccacctctcc agtgtgtat gccaccaggc taccctcac 5100
ctacactctc acatggcagg gccaccccag cctctgttct cgtccacaca gtccctcacct 5160
cctatctcct tccattcccg ggcagggtgca gcttccccag gccaccttcc ctctcatcca 5220
gcccccccg tggcccctac tcagggggca agtccacta gctgccctga gttggtggtg 5280
ccctatgtcc ctacactca cagacgtttc cccaaccaga caggaaggcc caagggcagg 5340
accagcccc accttctccc actgcagcgc agccacgcac aggtgggctc catgacagcc 5400
cgggccggca gagcccttcc ctccctccag gccaggggc tccccgcagg cccacaggac 5460
tcccactcct tcccacctc ggcgtgggt gagccagagt ctgtcactca cctgtgtgtc 5520
accagtgagc gcatcaggac caggaaggtg agtaagcagg acaagaccaa ggctgagatg 5580
tagca 5585

```

<210> 7

<211> 670

<212> PRT

<213> Mus musculus retinoic acid-responsive protein (Stra6) mRNA,
complete cds (translated), GenBank AF062476

<400> 7

Met Glu Ser Gln Ala Ser Glu Asn Gly Ser Gln Thr Ser Ser Gly Val
1 5 10 15

Thr Asp Asp Tyr Ser Ser Trp Tyr Ile Glu Glu Pro Leu Gly Ala Glu
20 25 30

Glu Val Gln Pro Glu Gly Val Ile Pro Leu Cys Gln Leu Thr Ala Pro
35 40 45

Pro Ala Leu Leu His Ala Cys Leu Ala Ser Leu Ser Phe Leu Val Leu
50 55 60

Leu Leu Leu Ala Leu Leu Val Arg Arg Arg Arg Leu Trp Pro Arg Cys
65 70 75 80

Gly His Arg Gly Leu Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly
85 90 95

Asp Leu Ser Trp Thr Val Pro Ala Ala Val Phe Val Val Leu Phe Ser
100 105 110

Asn Leu Cys Leu Leu Leu Pro Asp Glu Asn Pro Leu Pro Phe Leu Asn
115 120 125

Leu Thr Ala Ala Ser Ser Pro Asp Gly Glu Met Glu Thr Ser Arg Gly
130 135 140

Pro Trp Lys Leu Leu Ala Leu Leu Tyr Tyr Pro Ala Leu Tyr Tyr Pro
145 150 155 160

Leu Ala Ala Cys Ala Ser Ala Gly His Gln Ala Ala Phe Leu Leu Gly
165 170 175

Thr Val Leu Ser Trp Ala His Phe Gly Val Gln Val Trp Gln Lys Ala
180 185 190

Glu Cys Pro Gln Asp Pro Lys Ile Tyr Lys His Tyr Ser Leu Leu Ala
 195 200 205

Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro
 210 215 220

Val Gln Leu Val Gln Ser Leu Arg His Arg Thr Gly Ala Gly Ser Gln
 225 230 235 240

Gly Leu Gln Thr Ser Tyr Ser Glu Lys Tyr Leu Arg Thr Leu Leu Cys
 245 250 255

Pro Lys Lys Leu Asp Ser Cys Ser His Pro Ala Ser Lys Arg Ser Leu
 260 265 270

Leu Ser Arg Ala Trp Ala Phe Ser His His Ser Ile Tyr Thr Pro Gln
 275 280 285

Pro Gly Phe Arg Leu Pro Leu Lys Leu Val Ile Ser Ala Thr Leu Thr
 290 295 300

Gly Thr Ala Thr Tyr Gln Val Ala Leu Leu Leu Leu Val Ser Val Val
 305 310 315 320

Pro Thr Val Gln Lys Val Arg Ala Gly Ile Asn Thr Asp Val Ser Tyr
 325 330 335

Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Arg Gln Glu Val
 340 345 350

Val Glu Leu Val Lys His His Leu Trp Thr Val Glu Ala Cys Tyr Ile
 355 360 365

Ser Ala Leu Val Leu Ser Cys Ala Ser Thr Phe Leu Leu Leu Ile Arg
 370 375 380

Ser Leu Arg Thr His Arg Ala Asn Leu Gln Ala Leu His Arg Gly Ala
 385 390 395 400

Ala Leu Asp Leu Asp Pro Pro Leu Gln Ser Ile His Pro Ser Arg Gln

405	410	415
Ala Ile Val Ser Trp Met Ser Phe Cys Ala Tyr Gln Thr Ala Phe Ser		
420	425	430
Cys Leu Gly Leu Leu Val Gln Gln Val Ile Phe Phe Leu Gly Thr Thr		
435	440	445
Ser Leu Ala Phe Leu Val Phe Val Pro Leu Leu His Gly Arg Asn Leu		
450	455	460
Leu Leu Leu Arg Ser Leu Glu Ser Thr Trp Pro Phe Trp Leu Thr Val		
465	470	475
Ala Leu Ala Val Ile Leu Gln Asn Ile Ala Ala Asn Trp Ile Phe Leu		
485	490	495
Arg Thr His His Gly Tyr Pro Glu Leu Thr Asn Arg Arg Met Leu Cys		
500	505	510
Val Ala Thr Phe Leu Leu Phe Pro Ile Asn Met Leu Val Gly Ala Ile		
515	520	525
Met Ala Val Trp Arg Val Leu Ile Ser Ser Leu Tyr Asn Thr Val His		
530	535	540
Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Gln Arg Ala Ala Ser Leu		
545	550	555
Asp Pro Gly Tyr His Thr Tyr Gln Asn Phe Leu Arg Ile Glu Ala Ser		
565	570	575
Gln Ser His Pro Gly Val Ile Ala Phe Cys Ala Leu Leu Leu His Ala		
580	585	590
Pro Ser Pro Gln Pro Arg Pro Pro Leu Ala Pro Gln Asp Ser Leu Arg		
595	600	605
Pro Ala Glu Glu Glu Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Leu		
610	615	620

Met Ala Lys Gly Ala Gly His Lys Gly Ser Gln Ser Arg Ala Arg Trp
625 630 635 640

Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Ser Leu Gln Ala Phe Arg
645 650 655

Lys Ala Ala Leu Thr Ser Ala Lys Ala Asn Gly Thr Gln Pro
660 665 670